

RAW SEQUENCE LISTING

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Application Serial Number: 10/516,558
Source: PCT
Date Processed by STIC: 1-26-06

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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/516,558

DATE: 01/26/2006

TIME: 09:10:00

Input Set : A:\3190-070 Sequence Listing.txt
 Output Set: N:\CRF4\01262006\J516558.raw

3 <110> APPLICANT: Chano, Tokuhiro
 4 Okabe, Hidetoshi
 5 Ikegawa, Shiro
 7 <120> TITLE OF INVENTION: RB1 gene induced protein (RB1CC1) and gene
 9 <130> FILE REFERENCE: 3190-070
 11 <140> CURRENT APPLICATION NUMBER: US 10/516,558
 12 <141> CURRENT FILING DATE: 2004-11-30
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/00882
 15 <151> PRIOR FILING DATE: 2003-01-30
 17 <150> PRIOR APPLICATION NUMBER: JP P2002-161400
 18 <151> PRIOR FILING DATE: 2002-06-03
 20 <150> PRIOR APPLICATION NUMBER: JP P2002-214978
 21 <151> PRIOR FILING DATE: 2002-07-24
 23 <160> NUMBER OF SEQ ID NOS: 132
 25 <170> SOFTWARE: PatentIn version 3.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1594
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Unknown
 32 <220> FEATURE:
 33 <223> OTHER INFORMATION: human RB1CC1
 35 <400> SEQUENCE: 1
 37 Met Lys Leu Tyr Val Phe Leu Val Asn Thr Gly Thr Thr Leu Thr Phe
 38 1 5 10 15
 41 Asp Thr Glu Leu Thr Val Gln Thr Val Ala Asp Leu Lys His Ala Ile
 42 20 25 30
 45 Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn
 46 35 40 45
 49 Gly Gly Glu Cys Met Ala Ala Asp Arg Arg Val Cys Thr Tyr Ser Ala
 50 50 55 60
 53 Gly Thr Asp Thr Asn Pro Ile Phe Leu Phe Asn Lys Glu Met Ile Leu
 54 65 70 75 80
 57 Cys Asp Arg Pro Pro Ala Ile Pro Lys Thr Thr Phe Ser Thr Glu Asn
 58 85 90 95
 61 Asp Met Glu Ile Lys Val Glu Glu Ser Leu Met Met Pro Ala Val Phe
 62 100 105 110
 65 His Thr Val Ala Ser Arg Thr Gln Leu Ala Leu Glu Met Tyr Glu Val
 66 115 120 125
 69 Ala Lys Lys Leu Cys Ser Phe Cys Glu Gly Leu Val His Asp Glu His
 70 130 135 140
 73 Leu Gln His Gln Gly Trp Ala Ala Ile Met Ala Asn Leu Glu Asp Cys
 74 145 150 155 160
 77 Ser Asn Ser Tyr Gln Lys Leu Leu Phe Lys Phe Glu Ser Ile Tyr Ser

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78	165	170	175
81	Asn Tyr Leu Gln Ser Ile Glu Asp Ile Lys Leu Lys Leu Thr His Leu		
82	180	185	190
85	Gly Thr Ala Val Ser Val Met Ala Lys Ile Pro Leu Leu Glu Cys Leu		
86	195	200	205
89	Thr Arg His Ser Tyr Arg Glu Cys Leu Gly Arg Leu Asp Ser Leu Pro		
90	210	215	220
93	Glu His Glu Asp Ser Glu Lys Ala Glu Thr Lys Arg Ser Thr Glu Leu		
94	225	230	235
97	240	245	250
98	255	260	265
101	Ser Phe Pro Lys Ser Val Glu His Val Ser Pro Asp Thr Ala Asp Ala		
102	270	275	280
105	Glu Ser Gly Lys Glu Ile Arg Glu Ser Cys Gln Ser Thr Val His Gln		
106	285	290	295
109	Gln Asp Glu Thr Thr Ile Asp Thr Lys Asp Gly Asp Leu Pro Phe Phe		
110	300	305	310
113	320	325	330
114	335	340	345
117	Val Glu Ser Leu Val Arg Lys Cys Phe Asp Ser Met Ser Arg Leu Asp		
118	350	355	360
121	365	370	375
122	380	385	390
125	395	400	405
126	410	415	420
128	425	430	435
129	440	445	450
132	455	460	465
133	470	475	480
136	485	490	495
137	505	510	515
140	520	525	530
141	535	540	545
144	550	555	560
145	555	560	565
148	570	575	580
149	585	590	595
152	600	605	610
153	615	620	625
156	630	635	640
157	645	650	655
160	660	665	670
161	675	680	685
164	690	695	700
165	705	710	715
168	720	725	730
169	735	740	745
172	750	755	760
173	765	770	775

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176 Ser Phe Cys Thr Gln Lys Pro Arg Lys Phe Asp Cys Glu Leu Pro Asp
177 565 570 575
180 Ile Ser Leu Lys Asp Leu Gln Phe Leu Gln Ser Phe Cys Pro Ser Glu
181 580 585 590
184 Val Gln Pro Phe Leu Arg Val Pro Leu Leu Cys Asp Phe Glu Pro Leu
185 595 600 605
188 His Gln His Val Leu Ala Leu His Asn Leu Val Lys Ala Ala Gln Ser
189 610 615 620
191 Leu Asp Glu Met Ser Gln Thr Ile Thr Asp Leu Leu Ser Glu Gln Lys
192 625 630 635 640
195 Ala Ser Val Ser Gln Thr Ser Pro Gln Ser Ala Ser Ser Pro Arg Met
196 645 650 655
199 Glu Ser Thr Ala Gly Ile Thr Thr Thr Ser Pro Arg Thr Pro Pro
200 660 665 670
203 Pro Leu Thr Val Gln Asp Pro Leu Cys Pro Ala Val Cys Pro Leu Glu
204 675 680 685
207 Glu Leu Ser Pro Asp Ser Ile Asp Ala His Thr Phe Asp Phe Glu Thr
208 690 695 700
211 Ile Pro His Pro Asn Ile Glu Gln Thr Ile His Gln Val Ser Leu Asp
212 705 710 715 720
215 Leu Asp Ser Leu Ala Glu Ser Pro Glu Ser Asp Phe Met Ser Ala Val
216 725 730 735
219 Asn Glu Phe Val Ile Glu Glu Asn Leu Ser Ser Pro Asn Pro Ile Ser
220 740 745 750
223 Asp Pro Gln Ser Pro Glu Met Met Val Glu Ser Leu Tyr Ser Ser Val
224 755 760 765
227 Ile Asn Ala Ile Asp Ser Arg Arg Met Gln Asp Thr Asn Val Cys Gly
228 770 775 780
231 Lys Glu Asp Phe Gly Asp His Thr Ser Leu Asn Val Gln Leu Glu Arg
232 785 790 795 800
235 Cys Arg Val Val Ala Gln Asp Ser His Phe Ser Ile Gln Thr Ile Lys
236 805 810 815
239 Glu Asp Leu Cys His Phe Arg Thr Phe Val Gln Lys Glu Gln Cys Asp
240 820 825 830
243 Phe Ser Asn Ser Leu Lys Cys Thr Ala Val Glu Ile Arg Asn Ile Ile
244 835 840 845
247 Glu Lys Val Lys Cys Ser Leu Glu Ile Thr Leu Lys Glu Lys His Gln
248 850 855 860
251 Lys Glu Leu Leu Ser Leu Lys Asn Glu Tyr Glu Gly Lys Leu Asp Gly
252 865 870 875 880
254 Leu Ile Lys Glu Thr Glu Glu Asn Glu Asn Lys Ile Lys Lys Leu Lys
255 885 890 895
258 Gly Glu Leu Val Cys Leu Glu Glu Val Leu Gln Asn Lys Asp Asn Glu
259 900 905 910
262 Phe Ala Leu Val Lys His Glu Lys Glu Ala Val Ile Cys Leu Gln Asn
263 915 920 925
266 Glu Lys Asp Gln Lys Leu Leu Glu Met Glu Asn Ile Met His Ser Gln
267 930 935 940
270 Asn Cys Glu Ile Lys Glu Leu Lys Gln Ser Arg Glu Ile Val Leu Glu

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271	945	950	955	960
274	Asp	Leu	Lys	Lys
275		Leu	His	Val
276			Glu	Asn
277			Asp	Glu
278			Lys	Leu
279			Gln	Leu
280			Ser	Glu
281			Leu	Gln
282			Ser	His
283			His	Leu
284			Lys	Glu
285			Leu	Leu
286			Glu	Glu
287			Leu	Lys
288			Lys	Glu
289			Asn	Gln
290			Gln	Gln
291			Ile	Glu
292			Asn	His
293			Gln	Ala
294			Ile	Glu
295			Glu	Ser
296			Leu	His
297			Gln	Glu
298			Ile	Leu
299			Glu	Lys
300			Leu	Leu
301			Glu	Glu
302			Leu	Asn
303			Glu	Gln
304			Asn	Gln
305			Gln	Ile
306			Glu	Glu
307			Leu	Leu
308			Glu	Glu
309			Leu	Leu
310			Glu	Glu
311			Leu	Asn
312			Gln	Gln
313			Ile	Lys
314			Glu	Ile
315			Asn	Glu
316			Tyr	Leu
317			Gln	Ala
318			Val	Glu
319			Gly	Leu
320			Leu	Ala
321			Glu	Glu
322			Ser	Ser
323			Asn	Asn
324			Ile	Ile
325			Glu	Glu
326			Leu	Leu
327			Gln	Gln
328			Ile	Ile
329			Glu	Glu
330			Ile	Ile
331			Glu	Glu
332			Leu	Leu
333			Gln	Gln
334			Iys	Iys
335			Asp	Asp
336			Glu	Glu
337			Lys	Lys
338			Tyr	Tyr
339			Glu	Glu
340			Ala	Ala
341			Ile	Ile
342			Ile	Ile
343			Gln	Gln
344			Ile	Ile
345			Glu	Glu
346			Asp	Asp
347			Glu	Glu
348			Leu	Leu
349			Glu	Glu
350			Arg	Arg
351			Glu	Glu
352			Val	Val
353			Glu	Glu
354			Lys	Lys
355			Leu	Leu
356			Glu	Glu
357			Asn	Asn
358			Gln	Gln
359			Ile	Ile
360			Ala	Ala
361			Glu	Glu
362			Gln	Gln
363			Leu	Leu
364			Glu	Glu
365			Asn	Asn
366			Glu	Glu
			Arg	Arg
			Thr	Thr
			Ser	Ser

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369 Leu Ile Ala Glu Gln Gln Thr Asn Phe Asn Thr Val Leu Thr Arg
 370 1325 1330 1335
 373 Glu Lys Met Arg Lys Glu Asn Ile Ile Asn Asp Leu Ser Asp Lys
 374 1340 1345 1350
 377 Leu Lys Ser Thr Met Gln Gln Gln Glu Arg Asp Lys Asp Leu Ile
 378 1355 1360 1365
 381 Glu Ser Leu Ser Glu Asp Arg Ala Arg Leu Leu Glu Glu Lys Lys
 382 1370 1375 1380
 385 Lys Leu Glu Glu Glu Val Ser Lys Leu Arg Ser Ser Ser Phe Val
 386 1385 1390 1395
 389 Pro Ser Pro Tyr Val Ala Thr Ala Pro Glu Leu Tyr Gly Ala Cys
 390 1400 1405 1410
 393 Ala Pro Glu Leu Pro Gly Glu Ser Asp Arg Ser Ala Val Glu Thr
 394 1415 1420 1425
 397 Ala Asp Glu Gly Arg Val Asp Ser Ala Met Glu Thr Ser Met Met
 398 1430 1435 1440
 401 Ser Val Gln Glu Asn Ile His Met Leu Ser Glu Glu Lys Gln Arg
 402 1445 1450 1455
 405 Ile Met Leu Leu Glu Arg Thr Leu Gln Leu Lys Glu Glu Glu Asn
 406 1460 1465 1470
 409 Lys Arg Leu Asn Gln Arg Leu Met Ser Gln Ser Met Ser Ser Val
 410 1475 1480 1485
 413 Ser Ser Arg His Ser Glu Lys Ile Ala Ile Arg Asp Phe Gln Val
 414 1490 1495 1500
 417 Gly Asp Leu Val Leu Ile Ile Leu Asp Glu Arg His Asp Asn Tyr
 418 1505 1510 1515
 421 Val Leu Phe Thr Val Ser Pro Thr Leu Tyr Phe Leu His Ser Glu
 422 1520 1525 1530
 425 Ser Leu Pro Ala Leu Asp Leu Lys Pro Gly Glu Gly Ala Ser Gly
 426 1535 1540 1545
 429 Ala Ser Arg Arg Pro Trp Val Leu Gly Lys Val Met Glu Lys Glu
 430 1550 1555 1560
 433 Tyr Cys Gln Ala Lys Lys Ala Gln Asn Arg Phe Lys Val Pro Leu
 434 1565 1570 1575
 437 Gly Thr Lys Phe Tyr Arg Val Lys Ala Val Ser Trp Asn Lys Lys
 438 1580 1585 1590
 441 Val
 446 <210> SEQ ID NO: 2
 447 <211> LENGTH: 1588
 448 <212> TYPE: PRT
 449 <213> ORGANISM: Unknown
 451 <220> FEATURE:
 452 <223> OTHER INFORMATION: mouse Rb1ccl
 454 <400> SEQUENCE: 2
 456 Met Lys Leu Tyr Val Phe Leu Val Asn Thr Gly Thr Thr Leu Thr Phe
 457 1 5 10 15
 460 Asp Thr Glu Leu Thr Val Gln Thr Val Ala Asp Leu Lys His Ala Ile
 461 20 25 30
 464 Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn

RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30
Seq#:31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54
Seq#:55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78
Seq#:79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101
Seq#:102,103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,119
Seq#:120,121,122,123,124,125,126,127,128,129,130,131,132

VERIFICATION SUMMARY

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